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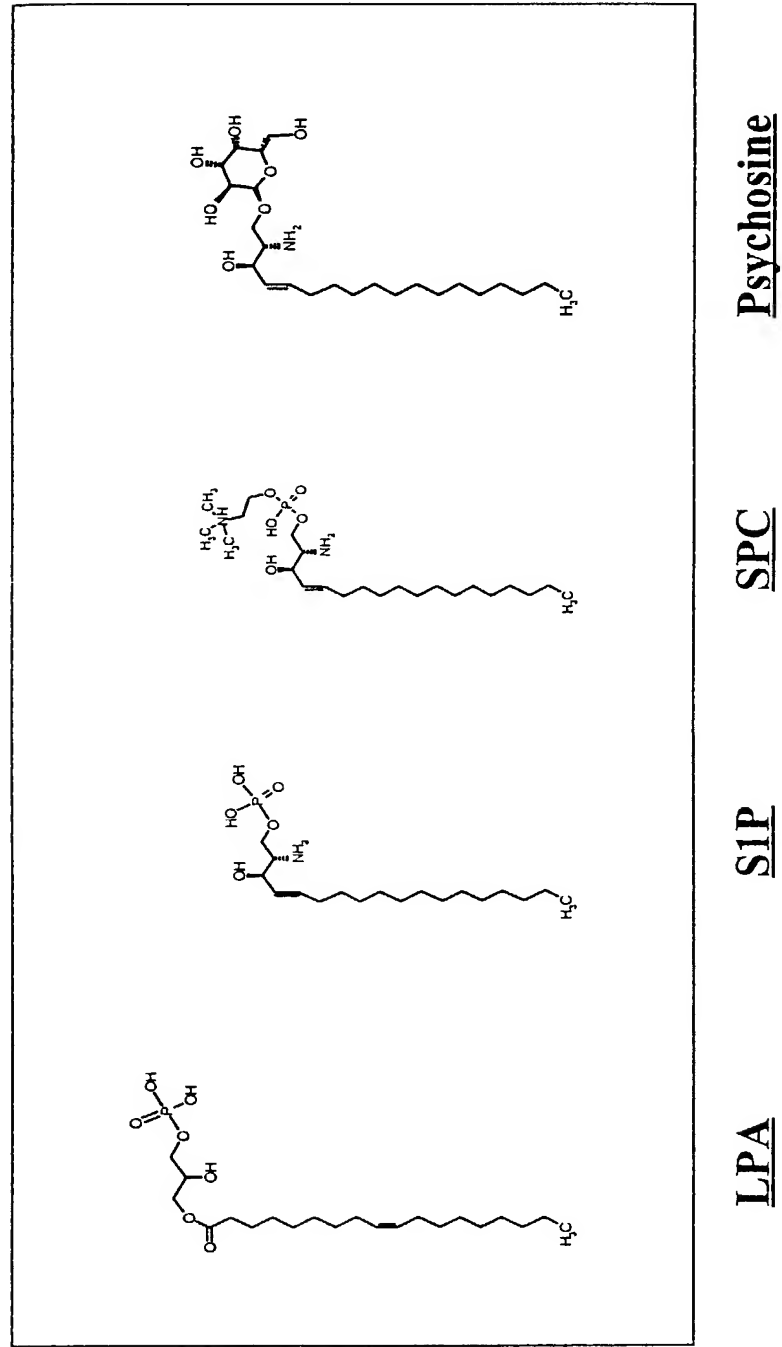


Figure 1B.

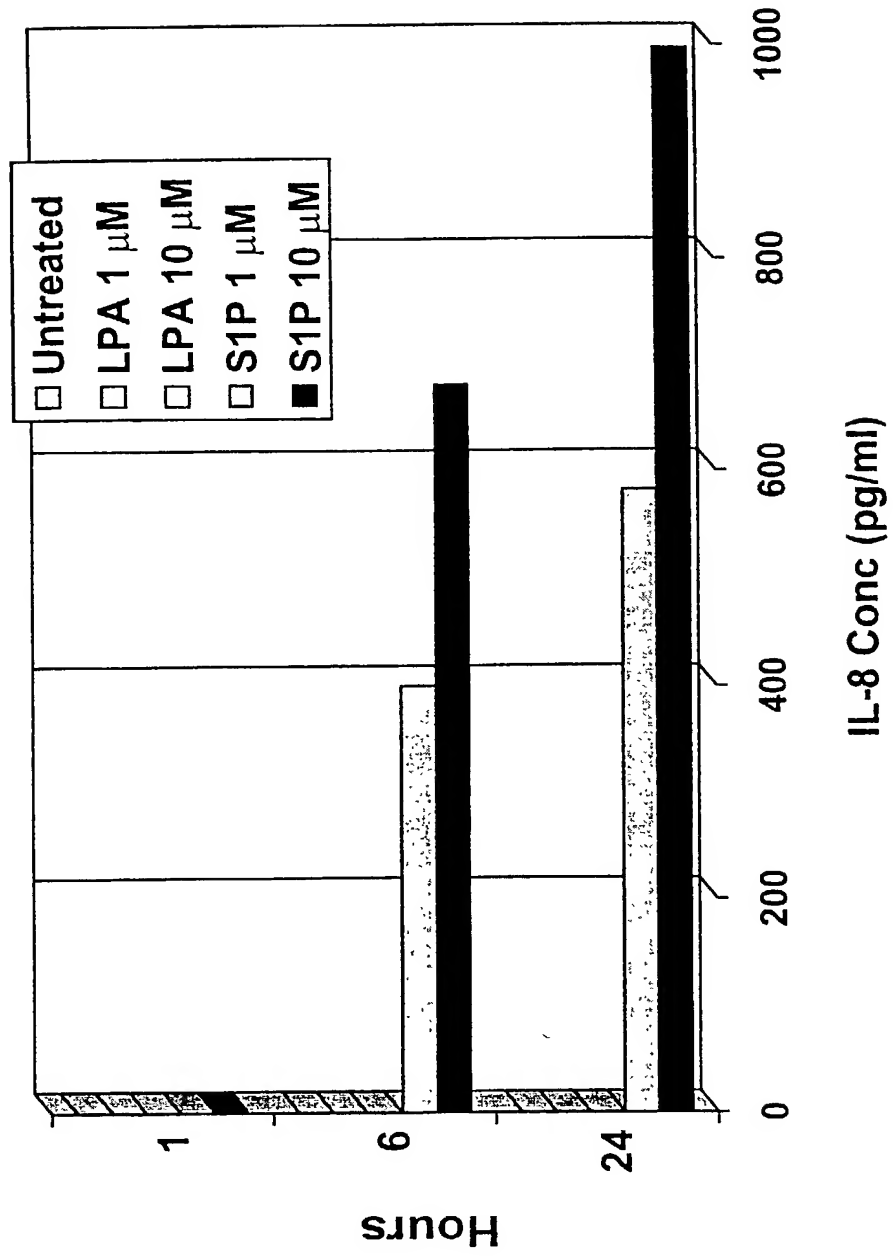


Figure 2A.

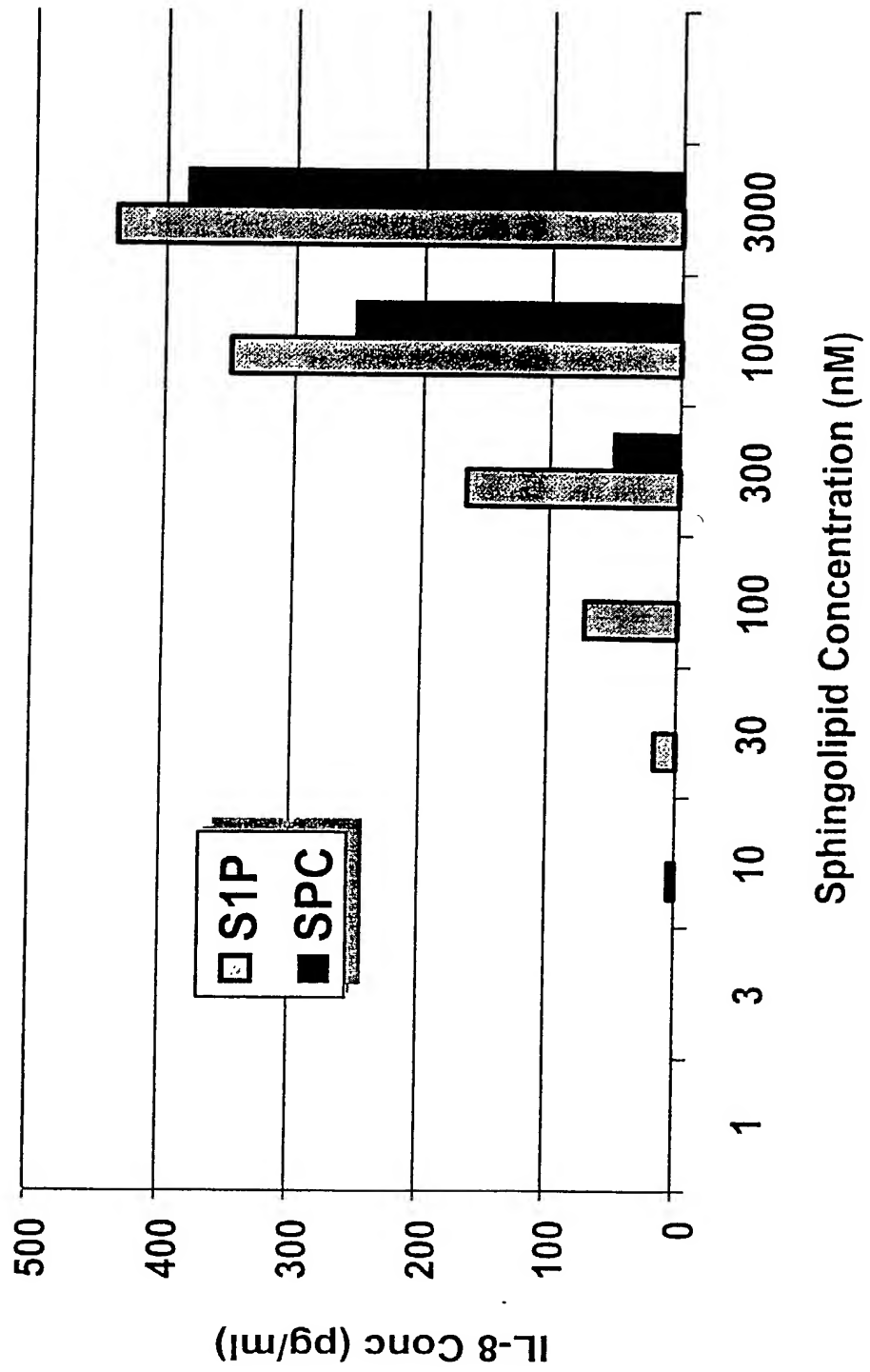
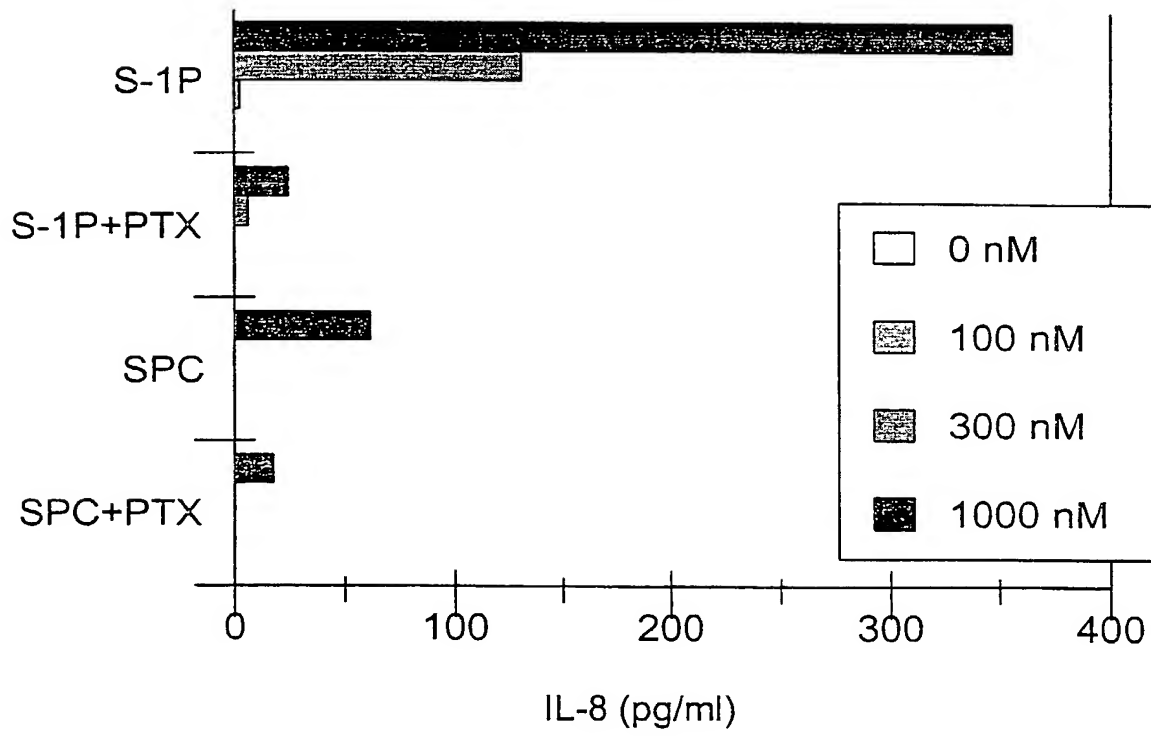


FIGURE 2 ~~8~~



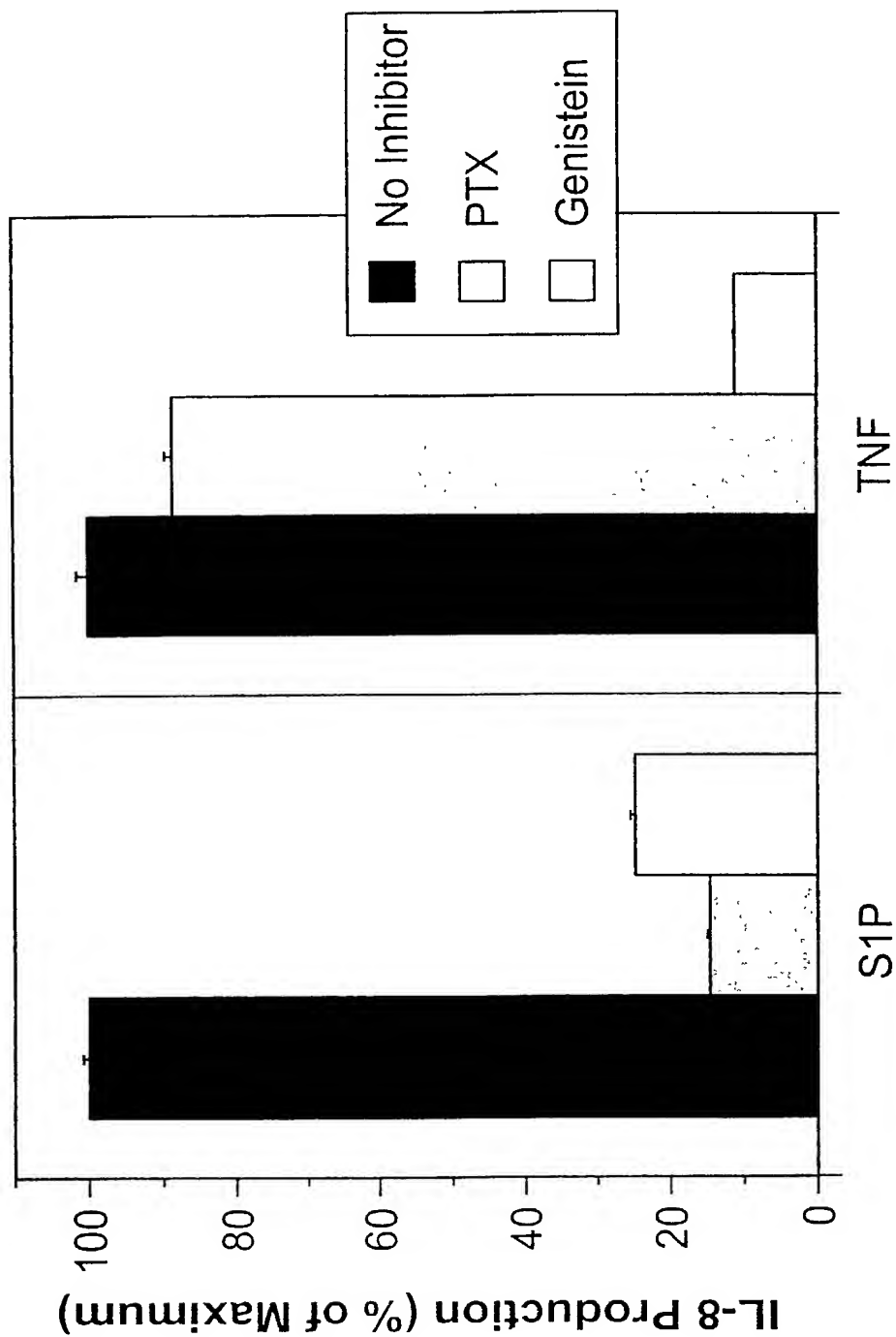


Figure 3.

FIGURE 4A

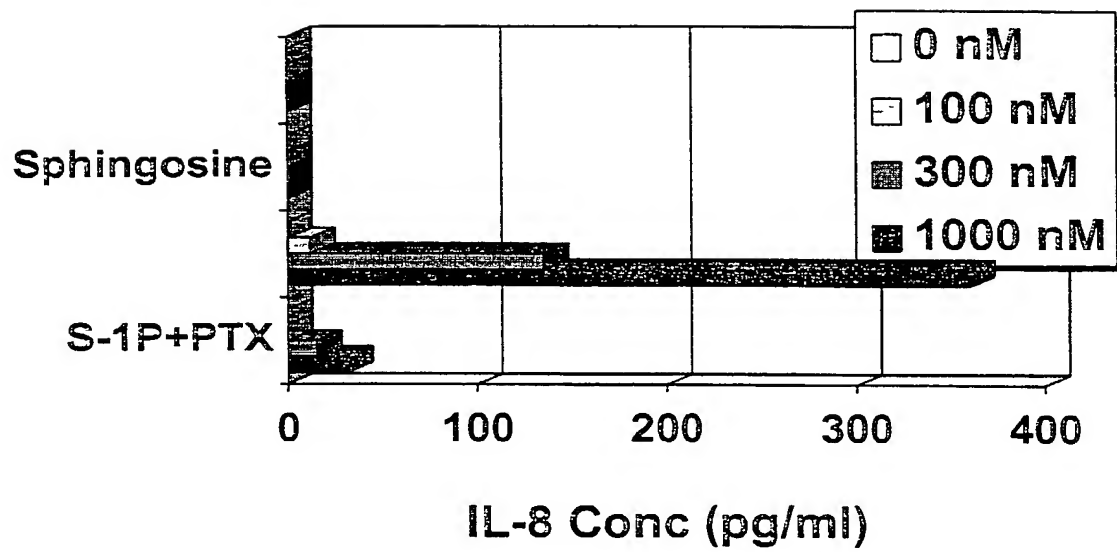


Figure 4B.

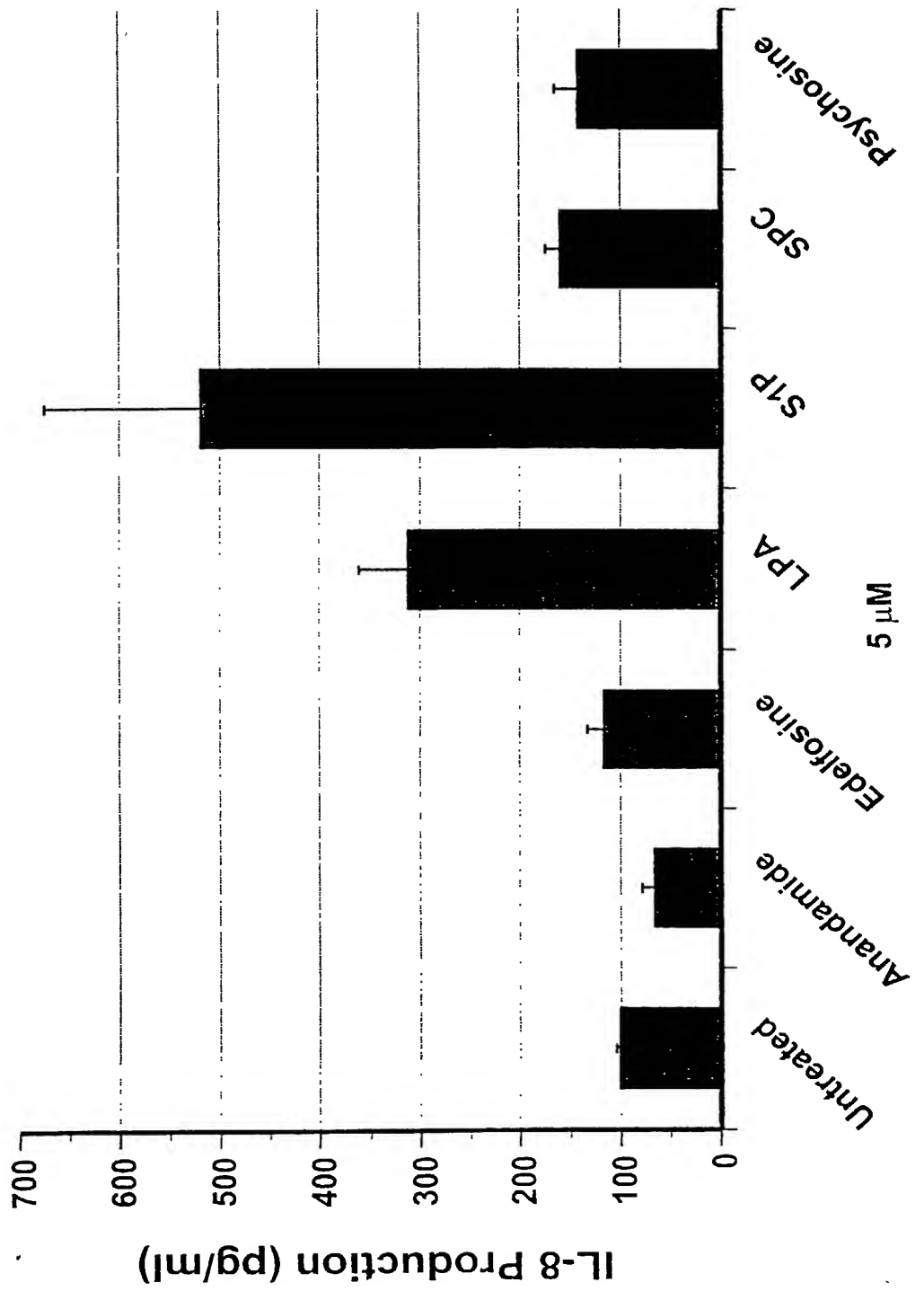


Figure 5.

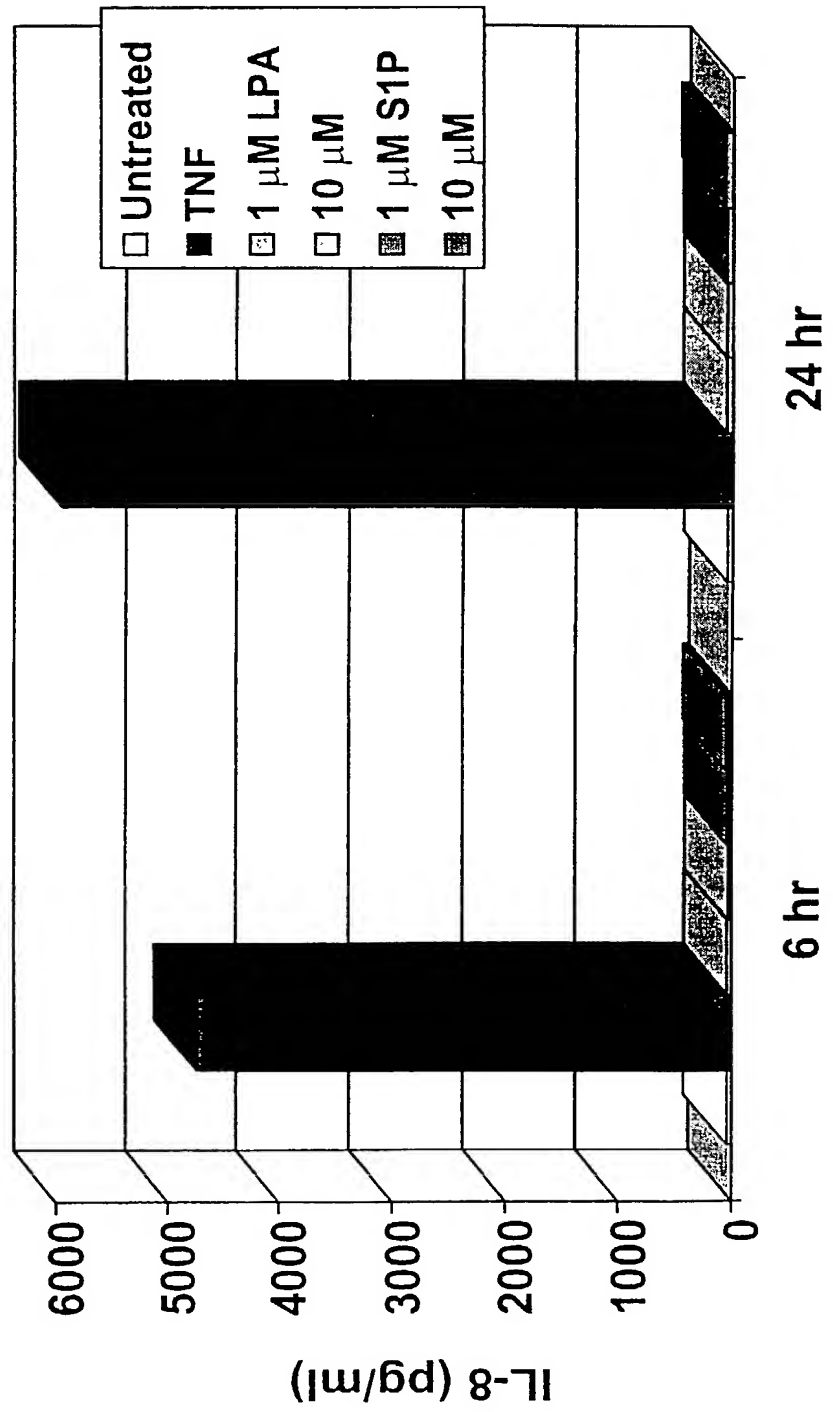
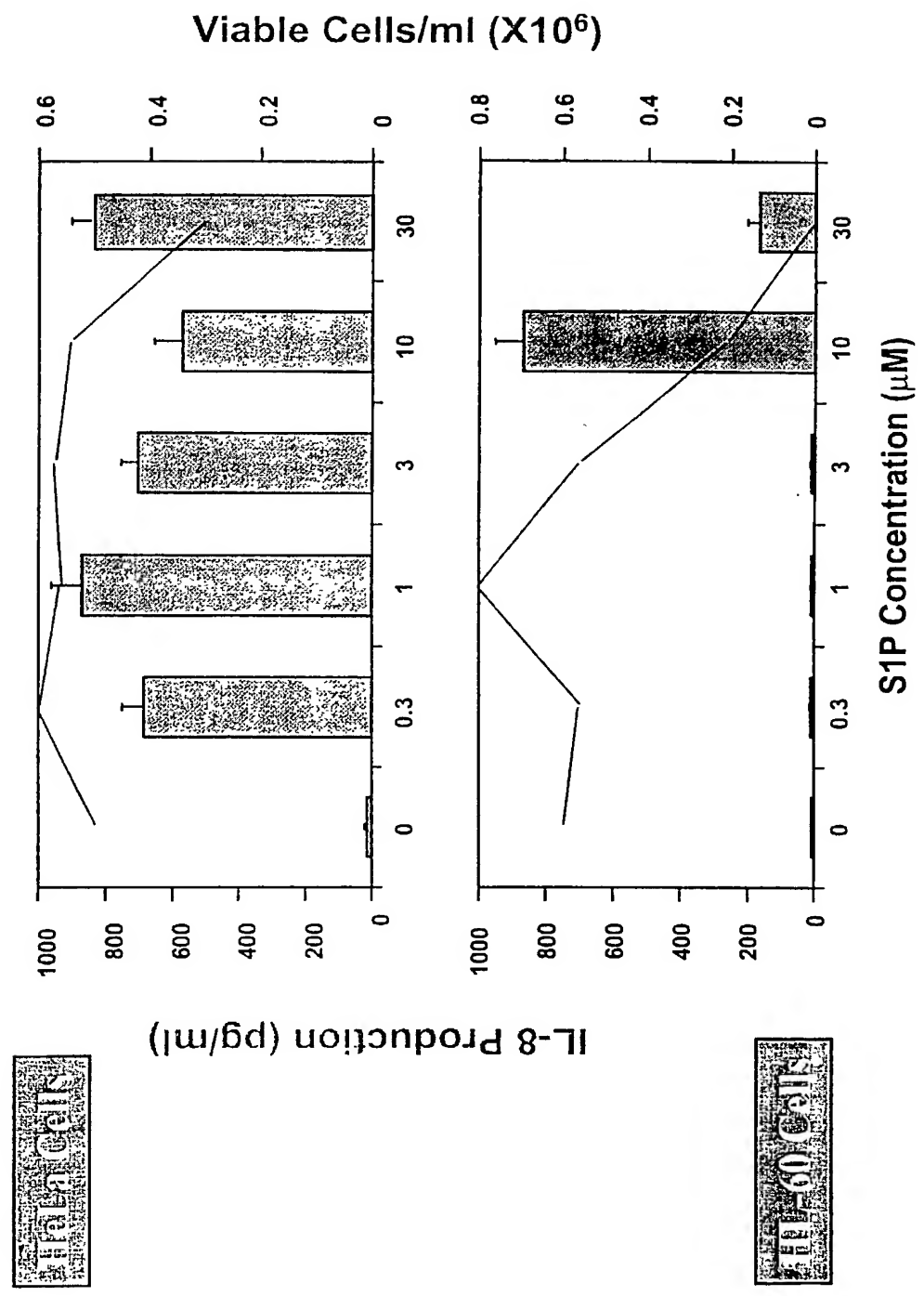




Figure 6.



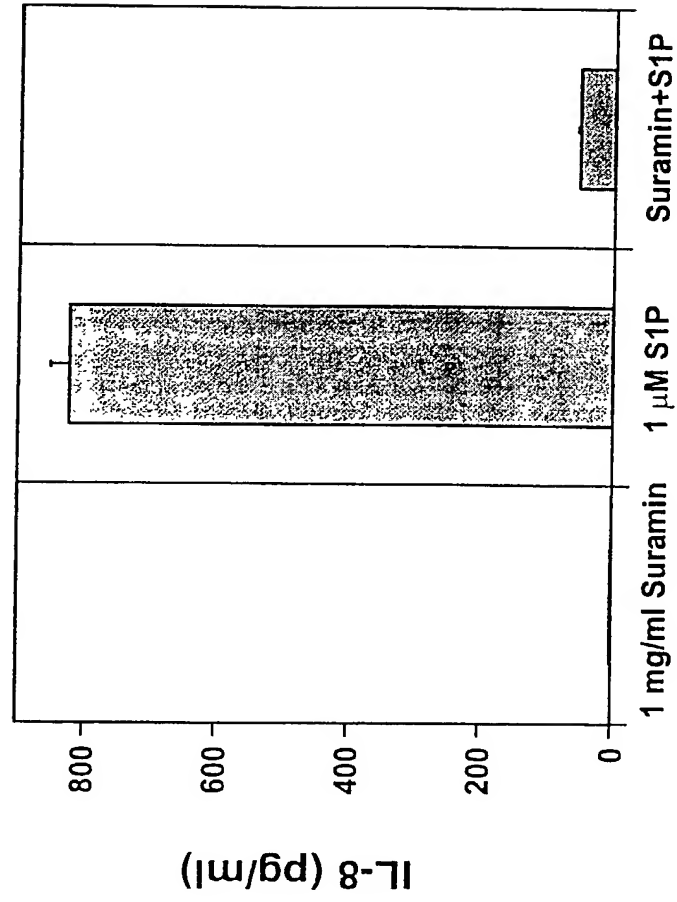


Figure 7.

Figure 8.

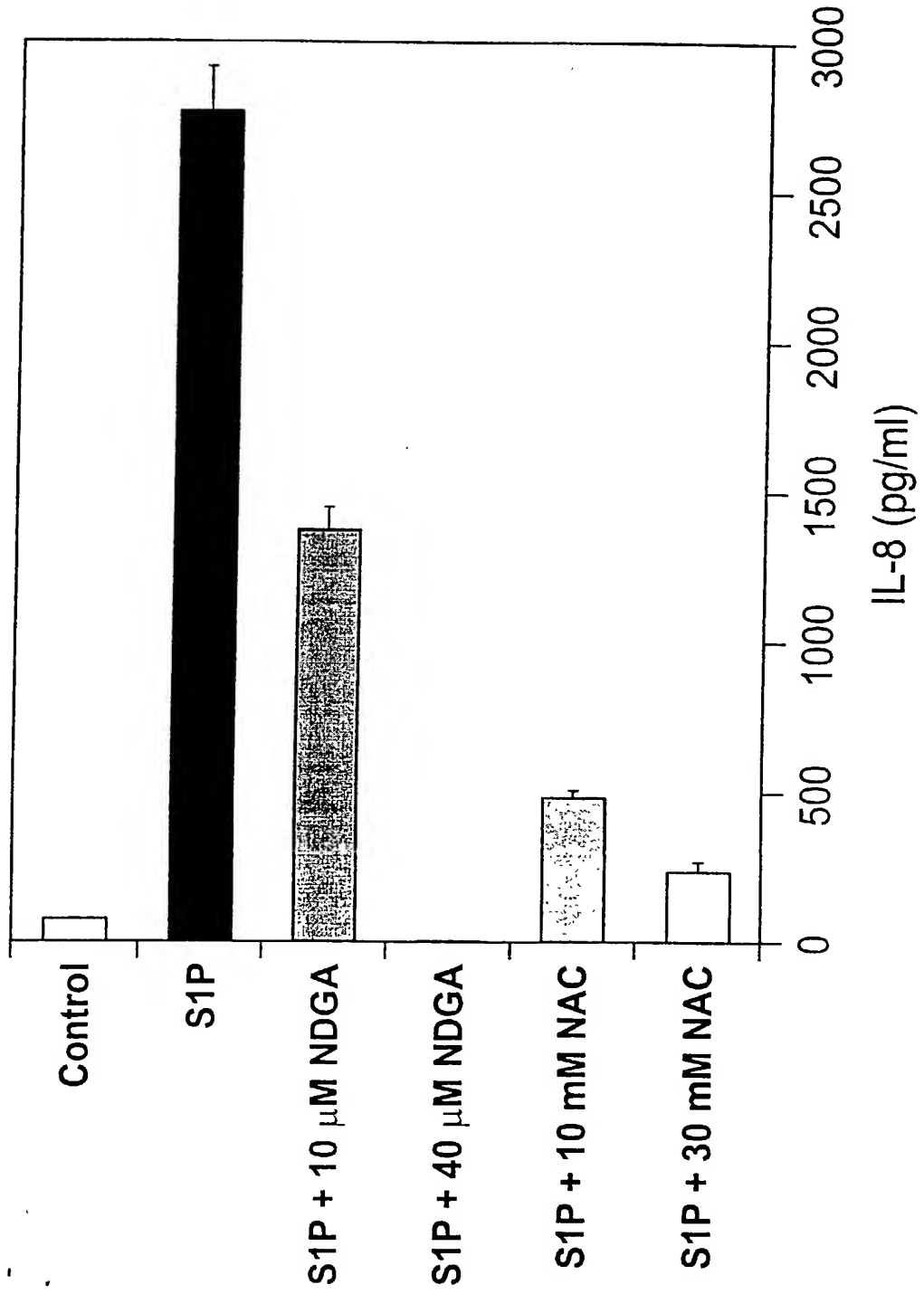


Figure 9.

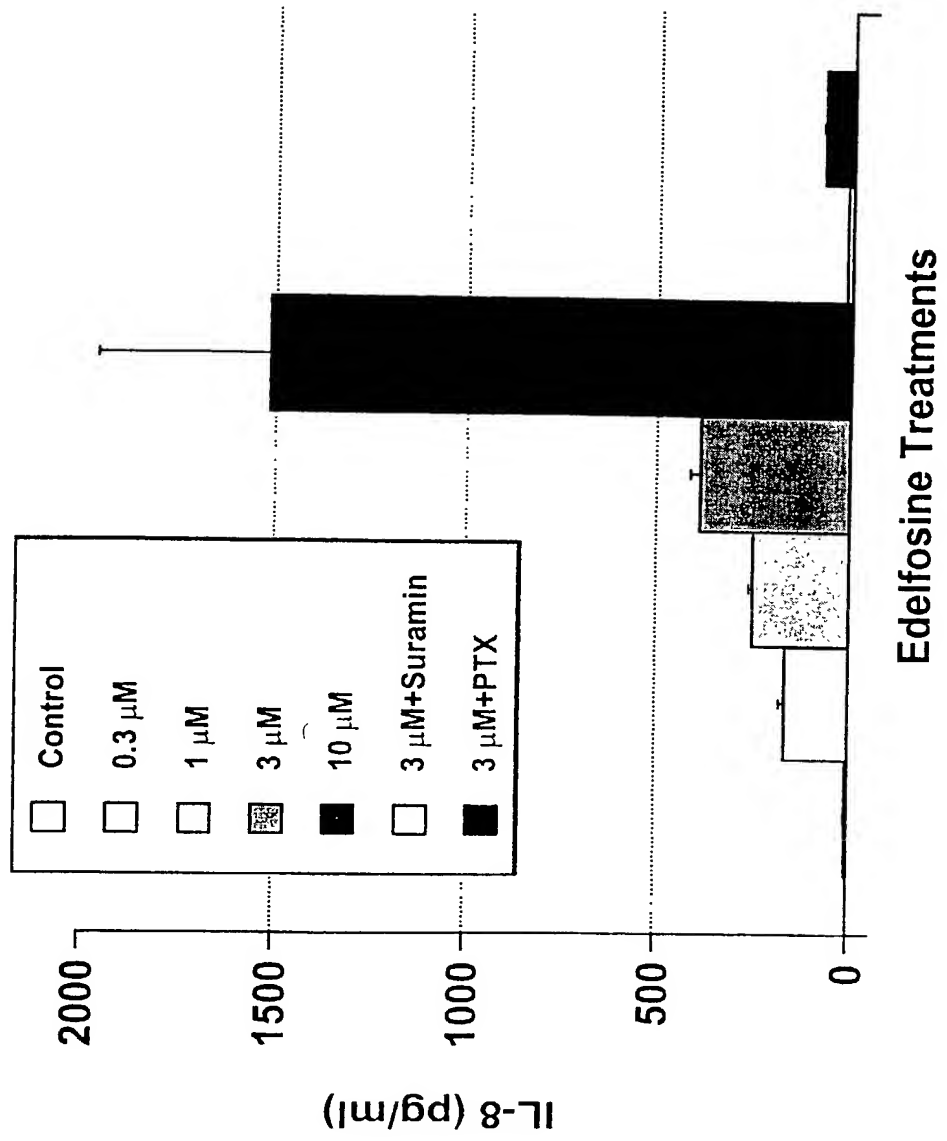


FIGURE 10A

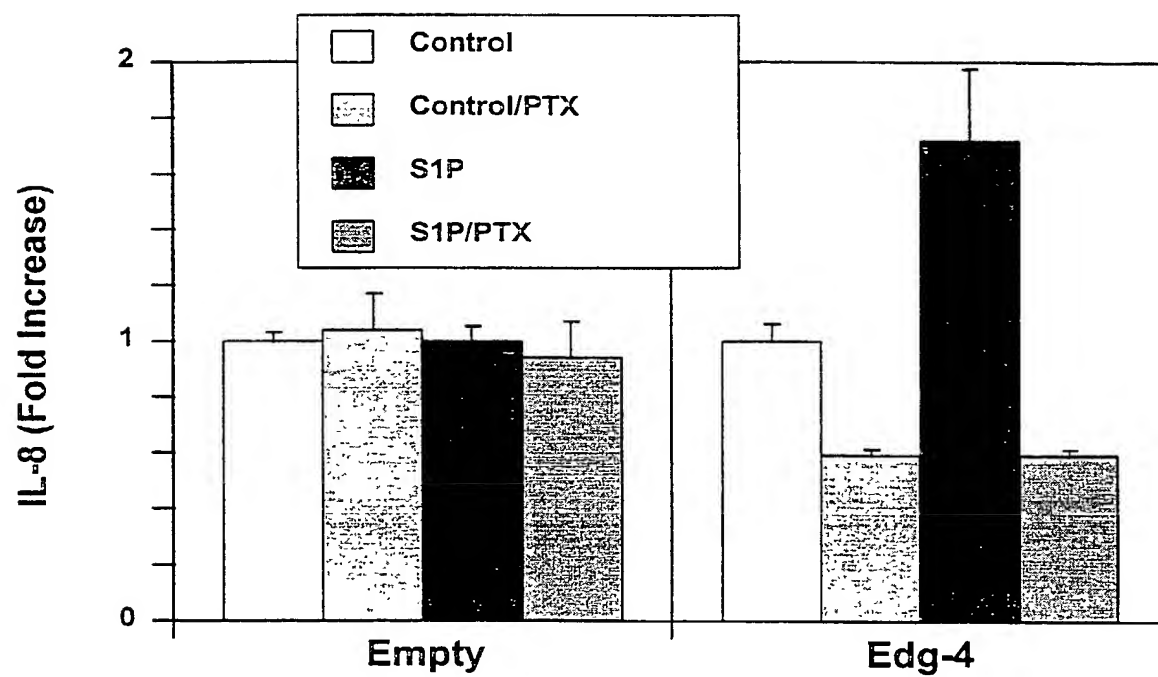


Figure 10B

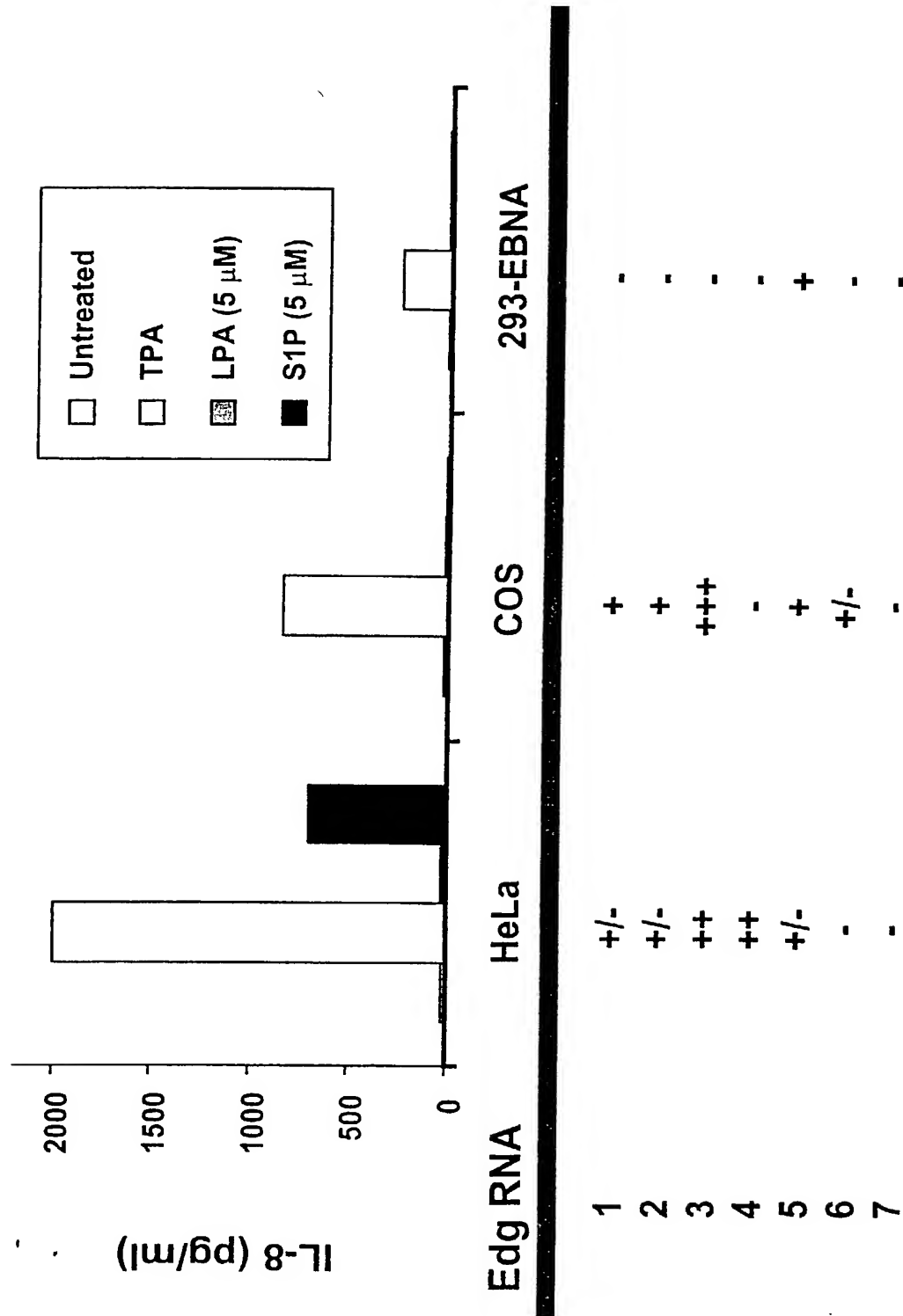


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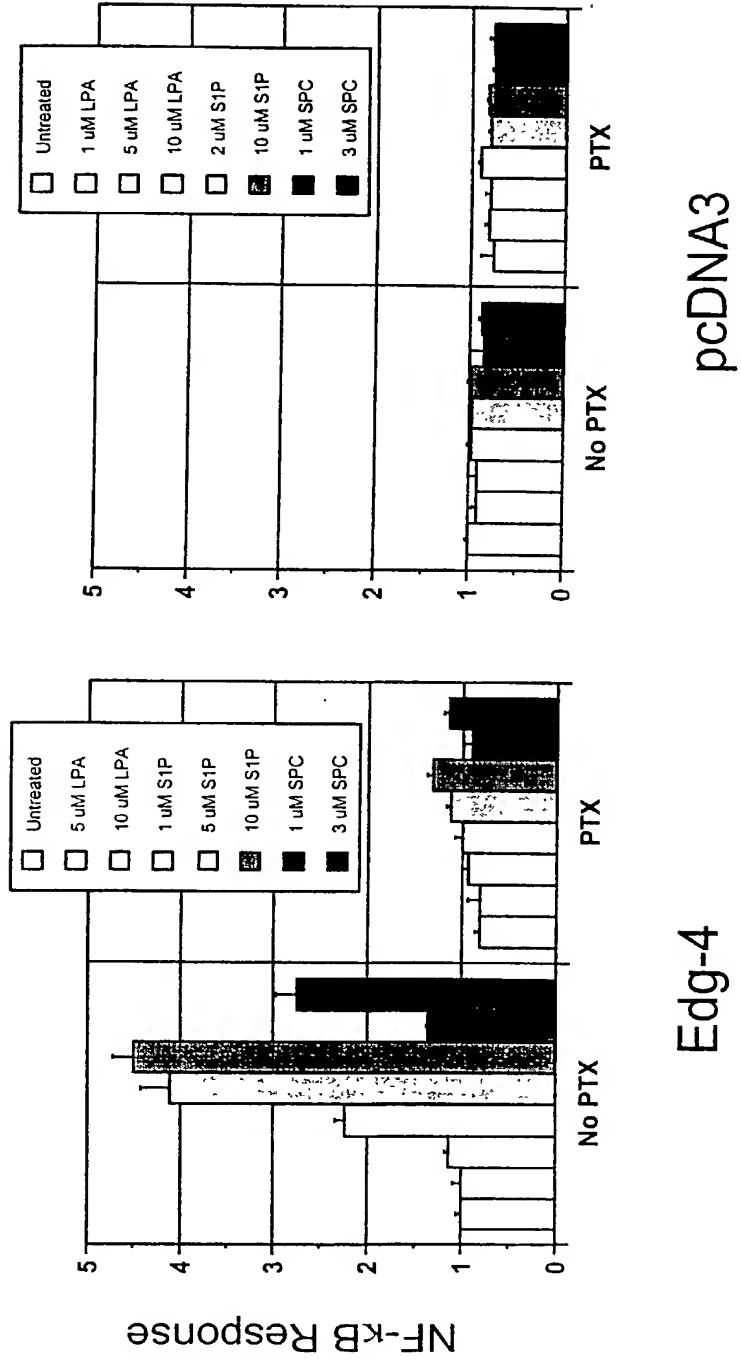


Figure 12.

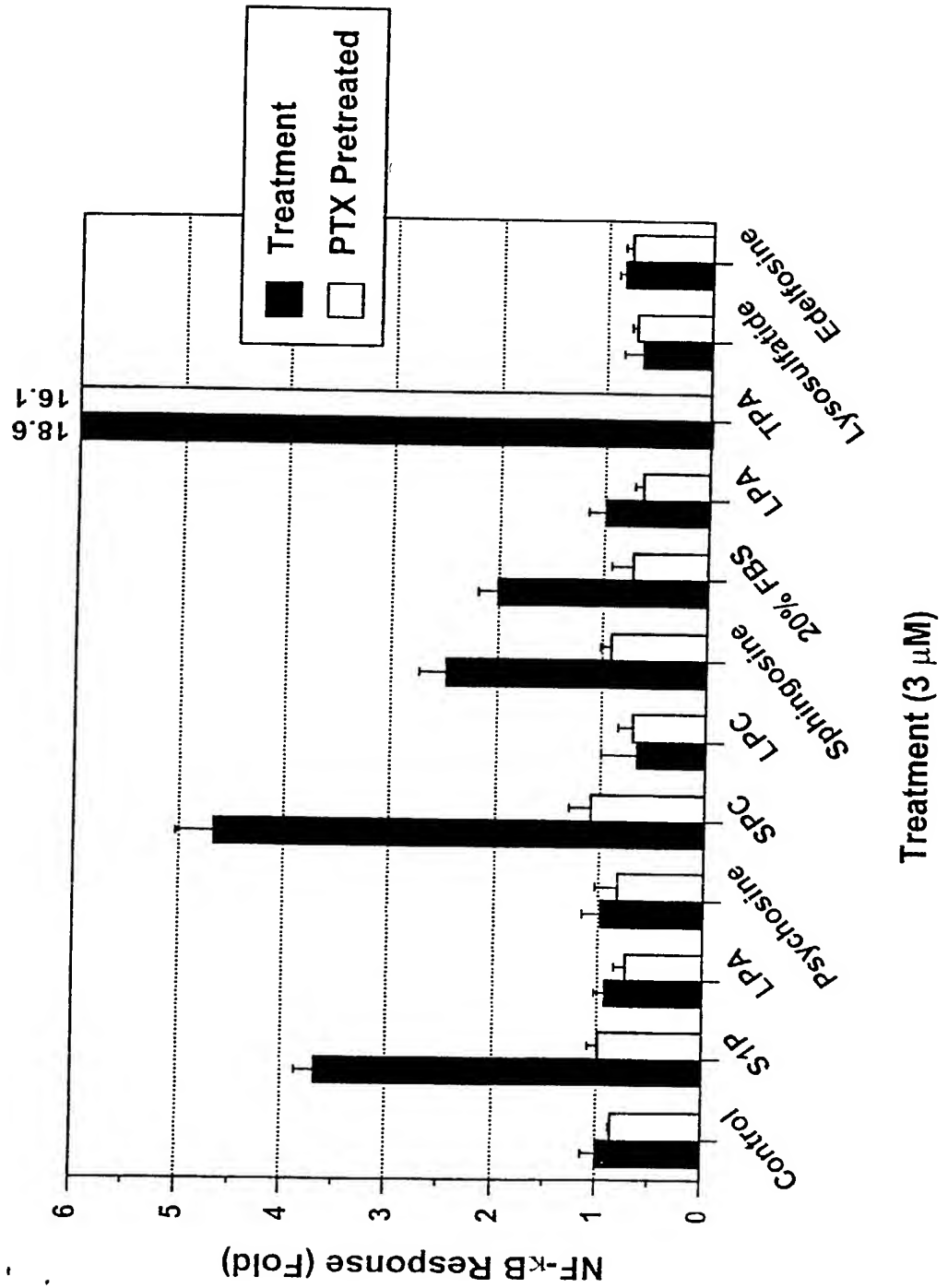




Figure 13.

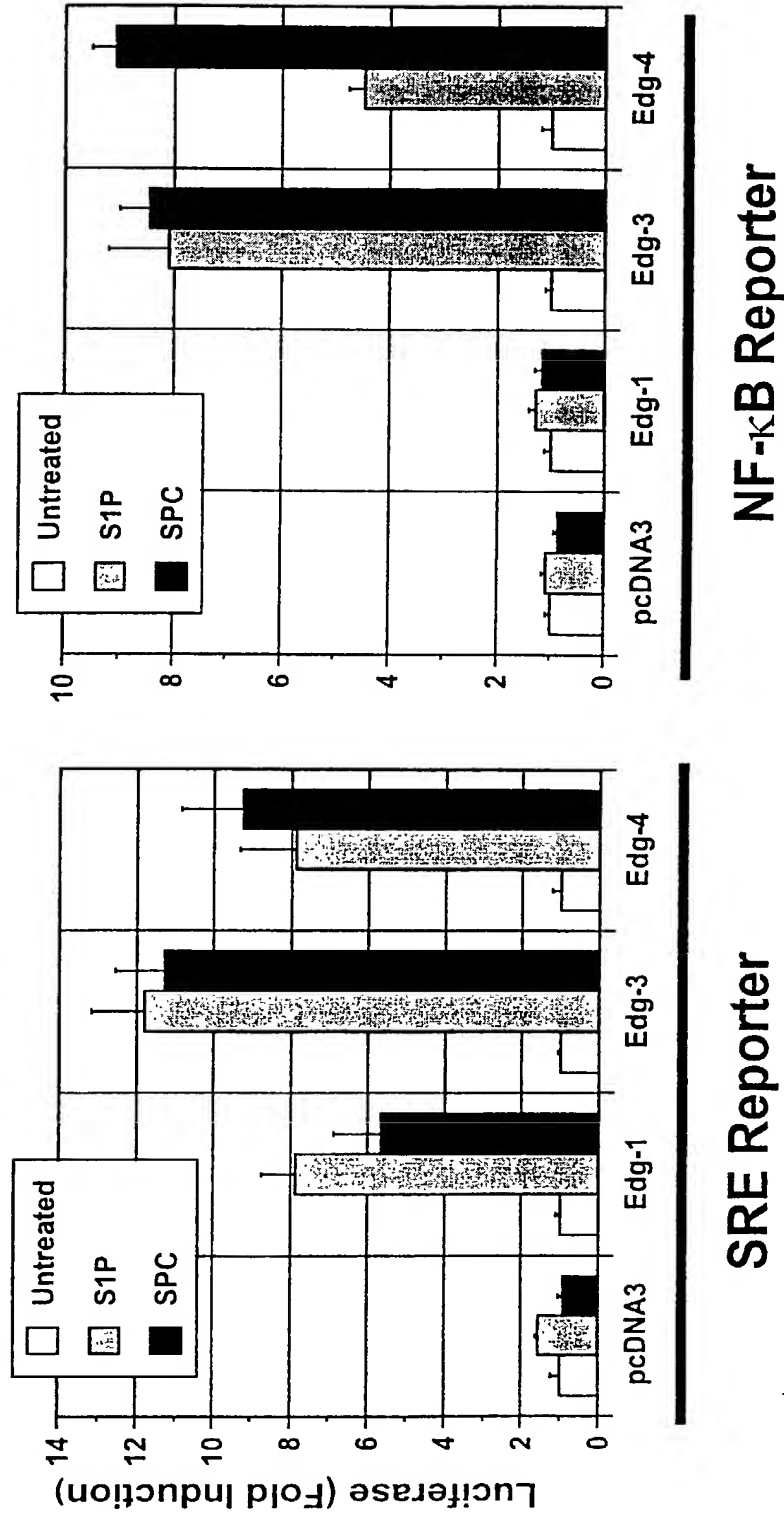


FIGURE 14

FIGURE 15 A

M G S L Y S E Y

```

1  AAAGCCCCATGGCCCCAGCAGGCCTCTGAGCCCCACCATGGGCAGCTTGTACTCGGAGTA
-----+-----+-----+-----+-----+-----+-----+
60 TTTTCGGGGTACCGGGGTTCGTCCGGAGACTCGGGGTGGTACCCGTCGAACATGAGCCTCAT

    L N P N K V Q E H Y N Y T K E T L E T Q
61 CCTGAACCCCAACAAGGTCCAGGAACACTATAATTATACCAAGGAGACGCTGGAAACGCA
-----+-----+-----+-----+-----+-----+-----+
120 GGACTTGGGGTTGTTCCAGGTCCTTGTGATATTAATATGGTTCCTCTGCGACCTTTGCGT

    E T T S R Q V A S A F I V I L C C A I V
121 GGAGACGACCTCCCGCCAGGTGGCCTCGGCCTTCATCGTCATCCTCTGTTGCGCCATTGT
-----+-----+-----+-----+-----+-----+-----+
180 CCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAGCAGTAGGAGACAACGCGGTAACA

    V E N L L V L I A V A R N S K F H S A M
181 GGTGGAACCTTCTGGTGCTCATTGCGGTGGCCCCGAAACAGCAAGTTCCTCTCGGCAAT
-----+-----+-----+-----+-----+-----+-----+
240 CCACCTTTTGGAAAGACCACGAGTAACGCCACCGGGCTTTGTCGTTCAAGGTGAGCCGTTA

    Y L F L G N L A A S D L L A G V A F V A
241 GTACCTGTTTCTGGGCAACCTGGCCGCTCCGATCTACTGGCAGGCGTGGCCTTCGTAGC
-----+-----+-----+-----+-----+-----+-----+
300 CATGGACAAAGACCCGTTGGACCGGCGGAGGCTAGATGACCGTCCGCACCGGAAGCATCG

    N T L L S G S V T L R L T P V Q W F A R
301 CAATACCTTGCTCTCTGGCTCTGTACGCTGAGGCTGACGCCTGTGCAGTGGTTTGCCCCG
-----+-----+-----+-----+-----+-----+-----+
360 GTTATGGAACGAGAGACCGAGACAGTGCGACTCCGACTGCGGACACGTACCAAACGGGC

    E G S A F I T L S A S V F S L L A I A I
361 GGAGGGCTCTGCCTTCATCACGCTCTCGGCCTCTGTCTTCAGCCTCCTGGCCATCGCCAT
-----+-----+-----+-----+-----+-----+-----+
420 CCTCCCAGACGGAAGTAGTGCGAGAGCCGAGACAGAAGTCGGAGGACCGGTAGCGGTA

    E R H V A I A K V K L Y G S D K S C R M
421 TGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTATGGCAGCGACAAGAGCTGCCGCAT
-----+-----+-----+-----+-----+-----+-----+
480 ACTCGCGGTGCACCGGTAACGGTTCAGTTCGACATACCGTCGCTGTTCTCGACGGCGTA

    L L L I G A S W L I S L V L G G L P I L
481 GCTTCTGCTCATCGGGGCTCGTGGCTCATCTCGCTGGTCCTCGGTGGCCTGCCCATCCT
-----+-----+-----+-----+-----+-----+-----+
540 CGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGACCAGGAGCCACCGGACGGGTAGGA

    G W N C L G H L E A C S T V L P L Y A K
541 TGGCTGGAACCTGCCTGGGCCACCTCGAGGCTGCTCCACTGTCTGCCTCTCTACGCCAA
-----+-----+-----+-----+-----+-----+-----+
600 ACCGACCTTGACGGACCCGGTGGAGCTCCGGACGAGGTGACAGGACGAGAGATGCGGTT

    H Y V L C V V T I F S I I L L A I V A L
601 GCATTATGTGCTGTGCGTGGTGACCATCTTCTCCATCATCCTGTTGGCCATCGTGGCCCT
-----+-----+-----+-----+-----+-----+-----+
660 CGTAATACAGACACGCACCACTGGTAGAAGAGGTAGTAGGACAACCGGTAGCACCGGGA

```

Y V R I Y C V V R S S H A D M A A P Q T  
 661 GTACGTGCGCATCTACTGCGTGGTCCGCTCAAGCCACGCTGACATGGCCGCCCCGAGAC 720  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 CATGCACGCGTAGATGACGCACCAGGCGAGTTCGGTGCGACTGTACCGGCGGGGCGTCTG  
  
 L A L L K T V T I V L G V F I V C W L P  
 721 GCTAGCCCTGCTCAAGACGGTCACCATCGTGCTAGGCGTCTTTATCGTCTGCTGGCTGCC 780  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 CGATCGGGACGAGTTCTGCCAGTGGTAGCACGATCCGCAGAAATAGCAGACGACCGACGG  
  
 A F S I L L L D Y A C P V H S C P I L Y  
 781 CGCCTTCAGCATCCTCCTTCTGGACTATGCCTGTCCCGTCCACTCCTGCCGATCCTCTA 840  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 GCGGAAGTCGTAGGAGGAAGACCTGATACGGACAGGGCAGGTGAGGACGGGCTAGGAGAT  
  
 K A H Y X F A V S T L N S L L N P V I Y  
 841 CAAAGCCCACTACYTTTTTCGCCGTCTCCACCCTGAATTCCCTGCTCAACCCCGTCATCTA 900  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 GTTTCGGGTGATGRAAAAGCGGCAGAGGTGGGACTTAAGGGACGAGTTGGGGCAGTAGAT  
  
 T W R S R D L R R E V L R P L Q C W R P  
 901 CACGTGGCGCAGCCGGGACCTGCGGCGGGAGGTGCTTCGGCCGCTGCAGTGCTGGCGGCC 960  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 GTGCACCGCGCTCGGCCCTGGACGCCGCCCTCCACGAAGCCGGCGACGTNACGACCGCCGG  
  
 G V G V Q G R R R G G T P G H H L L P L  
 961 GGGGGTGGGGGTGCAAGGACGGAGGCGGGGCGGGACCCCGGGCCACCACCTCCTGCCACT 1020  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 CCCCCACCCCCACGTTCTGCCTCCGCCCCGCCCTGGGGCCCCGGTGGTGGAGGACGGTGA  
  
 R S S S S L E R G M H M P T S P T F L E  
 1021 CCGCAGCTCCAGCTCCCTGGAGAGGGGCATGCACATGCCACGTCACCCACGTTTCTGGA 1080  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 GGCGTCGAGGTGAGGGACCTCTCCCCGTACGTGTACGGGTGCAGTGGGTGAAAAGACCT  
  
 G N T V V \*  
 1081 GGGCAACACGGTGGTCTGAGGGTGGGGTGGACCAACAACCAGGCCAGGGCATAGGGGTT 1140  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 CCCGTGTGCCACCAGACTCCCACCCCCACCTGGTTGTTGGTCCGGTCCCGTATCCCCAA  
  
 CATGGAAAGGCCACTGGGTGACCCCAAATA  
 1141 -----+-----+-----+-----+-----+ 1170  
 GTACCTTTCCGGTGACCCACTGGGGTTTAT

**Figure 15B**

**cDNA sequence of clone pC3-hedg4#36 encoding functional HEDG4 receptor protein.**

```

1  ATGGGCAGCTTGTACTCGGAGTACCTGAACCCCAACAAGGTCCAGGAACACTATAATTAT  60
   -----+-----+-----+-----+-----+-----+
TACCCGTCGAACATGAGCCTCATGGACTTGGGGTTGTTCCAGGTCCTTGTGATATTAATA

61  ACCAAGGAGACGCTGGAAACGCAGGAGACGACCTCCCGCCAGGTGGCCTCGGCCCTTCATC  120
   -----+-----+-----+-----+-----+-----+
TGGTTCCTCTGCGACCTTTGCGTCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAG

121  GTCATCCTCTGTTGCGCCATTGTGGTGGAAAACCTTCTGGTGCTCATTGCGGTGGCCCCGA  180
   -----+-----+-----+-----+-----+-----+
CAGTAGGAGACAACGCGGTAACACCACCTTTTGGGAAGACCACGAGTAACGCCACCGGGCT

181  AACAGCAAGTTCCTACTCGGCAATGTACCTGTTTCTGGGCAACCTGGCCGCCTCCGATCTA  240
   -----+-----+-----+-----+-----+-----+
TTGTCGTTCAAGGTGAGCCGTTACATGGACAAAGACCCGTTGACCGGCGGAGGCTAGAT

241  CTGGCAGGCGTGGCCTTCGTAGCCAATACCTTGCTCTCTGGCTCTGTCACGCTGAGGCTG  300
   -----+-----+-----+-----+-----+-----+
GACCGTCCGCACCGGAAGCATCGGTTATGGAACGAGAGACCGAGACAGTGCGACTCCGAC

301  ACGCCTGTGCAGTGGTTTGGCCGGGAGGGCTCTGCCTTCATCACGCTCTCGGCCTCTGTC  360
   -----+-----+-----+-----+-----+-----+
TGCGGACACGTACCAAACGGGCCCTCCCGAGACGGAAGTAGTGCGAGAGCCGGAGACAG

361  TTCAGCCTCCTGGCCATCGCCATTGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTAT  420
   -----+-----+-----+-----+-----+-----+
AAGTCGGAGGACCGGTAGCGGTAACCTCGCGGTGCACCGGTAACGGTTCCAGTTCGACATA

421  GGCAGCGACAAGAGCTGCCGCATGCTTCTGCTCATCGGGGCCTCGTGGCTCATCTCGCTG  480
   -----+-----+-----+-----+-----+-----+
CCGTCGCTGTTCTCGACGGCGTACGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGAC

481  GTCCTCGGTGGCCTGCCCATCCTTGCTGGAAGTGCCTGGGCCACCTCGAGGCCTGCTCC  540
   -----+-----+-----+-----+-----+-----+
CAGGAGCCACCGGACGGGTAGGAACCGACCTTGACGGACCCGGTGGAGCTCCGGACGAGG

541  ACTGTCCTGCCTCTCTACGCCAAGCATTATGTGCTGTGCGTGGTGACCATCTTCTCCATC  600
   -----+-----+-----+-----+-----+-----+
TGACAGGACGGAGAGATGCGGTTGTAATACACGACACGCACCACTGGTAGAAGAGGTAG

601  ATCCTGTTGGCCGTCGTGGCCCTGTACGTGCGCATCTACTGCGTGGTCCGCTCAAGCCAC  660
   -----+-----+-----+-----+-----+-----+
TAGGACAACCGGCAGCACCGGGACATGCACGCGTAGATGACGCACCAGGCGAGTTCGGTG

661  GCTGACATGGCCGCCCCGACAGCGCTAGCCCTGCTCAAGACGGTCACCATCGTGCTAGGC  720
   -----+-----+-----+-----+-----+-----+
CGACTGTACC GGCGGGGCGTCTGCGATCGGGACGAGTTCTGCCAGTGGTAGCACGATCCG

721  GTCTTTATCGTCTGCTGGCTGCCCCGCTTCAGCATCCTCCTTCTGGACTATGCCTGTCCC  780
   -----+-----+-----+-----+-----+-----+

```



## FIGURE 16 A

```

1  MGSLYSEYLN PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE
51  NLLVLIAVAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL
151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
201 ILLAIVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAF
251 SILLLDYACP VHSCPILYKA HYXFAVSTLN SLLNPVIYTW RSRDLRREVL
301 RPLQCWRPGV GVQGRRRGGT PGHHLLPLRS SSSLERGMHM PTSPTFLEGN
351 TVV*

```

Conserved features of G-protein coupled receptors include:

N-terminal extracellular domain:	Residues 1 - 36
TM-I:	Residues 37 - 57
Intracellular loop 1:	Residues 58 - 68
TM-II:	Residues 69 - 92
Extracellular loop 1:	Residues 93 - 111
TM-III:	Residues 112 - 130
Intracellular loop 2:	Residues 131 - 149
TM-IV:	Residues 150 - 168
Extracellular loop 2:	Residues 169 - 185
TM-V:	Residues 186 - 210
Intracellular loop 3:	Residues 211 - 232
TM-VI:	Residues 233 - 254
Extracellular loop 3:	Residues 255 - 266
TM-VII:	Residues 267 - 285
C-terminal cytoplasmic domain:	Residues 286 - 353

Potential post-transcriptional modification sites:

N-glycosylation:	Residues 19
Phosphorylation:	Residues 142, 145, 219, 289, 332, 345
Myristylation:	Residues 141, 318

**Figure 16B**

**Predicted amino acid sequence of HEDG4 polypeptide encoded by pC3-hedg4#36.**

```
1  MGSLYSEYLN PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE
51  NLLVLIAVAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL
151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
201 ILLAVVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAF
251 SILLLDYACP VHSCPILYKA HYLFAVSTLN SLLNPVIYTW RSRDLRREVL
301 RPLQCWRPGV GVQGRRRGGT PGHHLLPLRS SSSLERGMHM PTSPTFLEGN
351 TVV
```



FIGURE 17 A

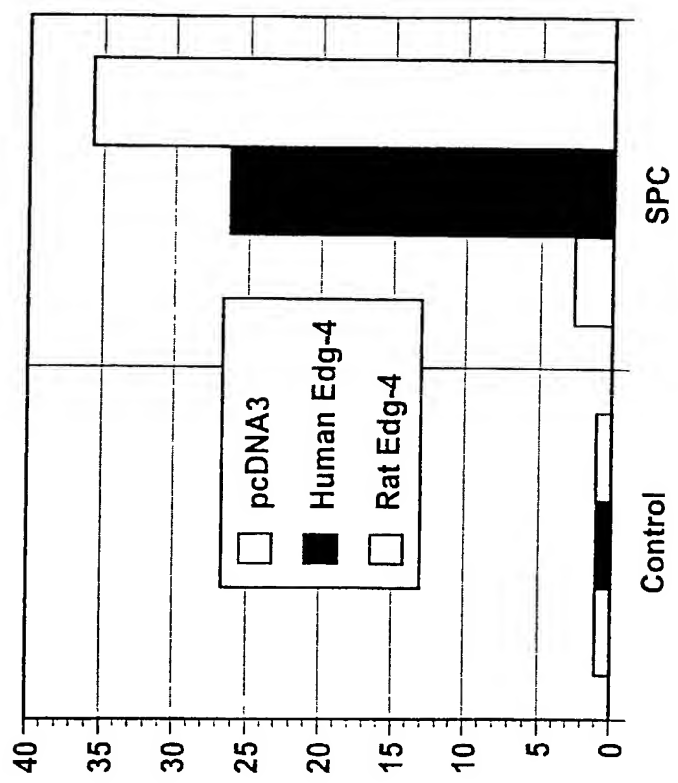
Human	1	MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVE	50
		:          :	
Rat	1	MGGLYSEYLNPEKVQEHYNYTKETLDMQETPSRKVASAFIILCCAIVVE	50
Human	51	NLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRL	100
Rat	51	NLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSL	100
Human	101	TPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVLYGSDKSCRMLL	150
		.   :	
Rat	101	TPLQWFAREGSAFITLSASVFSLLAIAIERQVAIAKVLYGSDKSCRMLM	150
Human	151	LIGASWLISLVLGGLPILGWNCLGHLEACSTVLPYAKHYVLCVVTIFSI	200
		:   :	
Rat	151	LIGASWLISLILGGLPILGWNCLDHLEACSTVLPYAKHYVLCVVTIFSV	200
Human	201	ILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLGVFIVCWLPAP	250
		:	
Rat	201	ILLAIVALYVRIYFVVRSSHADVAGPQTLALLKTVTIVLGVFIICWLPAF	250
Human	251	SILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL	300
		:	
Rat	251	SILLLDSTCPVRACPVLYKAHYFFAFATLNSLLNPVIYTWRSRDLRREVL	300
Human	301	RPLQCWRPGVGVGRRRGTPGHLLPLRSSSSLERGMHMPSTPTFLEGN	350
Rat	301	RPLLCWRQKGKATG.RRGGNPGHRLPLRSSSSLERGLHMPSTPTFLEGN	349
Human	351	TVV* 353	
Rat	350	TVV* 352	

Figure 17B

**Alignment of HEDG4 with pC3-hedg4#36 translation product and rat H218 (REDG4).** Differences between pC3-hedg4#36 translation product and previously determined HEDG4 polypeptide are indicated in reverse text. Differences between rat and human edg-4 polypeptide sequences are shown in bold, shaded text.

	1				50
HEDG4	MGS	LYSEYLN	PNKVQEHYNY	TKETLETQET	TSRQVASAFI VILCCAIVVE
HEDG4#36	MGS	LYSEYLN	PNKVQEHYNY	TKETLETQET	TSRQVASAFI VILCCAIVVE
REDG4	MGG	LYSEYLN	PEKVQEHYNY	TKETLDMQET	PSRKVASAFI IILCCAIVVE
	51				100
HEDG4	NLLVLI	AVAR	NSKFHSAMYL	FLGNLAASDL	LAGVAFVANT LLSGSVTLRL
HEDG4#36	NLLVLI	AVAR	NSKFHSAMYL	FLGNLAASDL	LAGVAFVANT LLSGSVTLRL
REDG4	NLLVLI	AVAR	NSKFHSAMYL	FLGNLAASDL	LAGVAFVANT LLSGPTVLSL
	101				150
HEDG4	TPVQWF	AREG	SAFITLSASV	FSLLAIAIER	HVAIAKVKLY GSDKSCRMLL
HEDG4#36	TPVQWF	AREG	SAFITLSASV	FSLLAIAIER	HVAIAKVKLY GSDKSCRMLL
REDG4	TPVQWF	AREG	SAFITLSASV	FSLLAIAIER	QVAIAKVKLY GSDKSCRMLM
	151				200
HEDG4	LIGASWL	LISL	VLGGLPILGW	NCLGHLEACS	TVLPLYAKHY VLCVVTIFSI
HEDG4#36	LIGASWL	LISL	VLGGLPILGW	NCLGHLEACS	TVLPLYAKHY VLCVVTIFSI
REDG4	LIGASWL	LISL	ELGGLPILGW	NCLDHLEACS	TVLPLYAKHY VLCVVTIFSV
	201				250
HEDG4	ILLAVVAL	YV	RIYCVVRSSH	ADMAAPQTLA	LLKTVTIVLG VFIVCWLPAP
HEDG4#36	ILLAVVAL	YV	RIYCVVRSSH	ADMAAPQTLA	LLKTVTIVLG VFIVCWLPAP
REDG4	ILLAI	VALYV	RIYFVVRSSH	ADVAGPQTLA	LLKTVTIVLG VFIIICWLPAP
	251				300
HEDG4	SILLLDY	ACP	VHSCPILYKA	HYXFAVSTLN	SLLNPVIYTW RSRDLRREVL
HEDG4#36	SILLLDY	ACP	VHSCPILYKA	HYXFAVSTLN	SLLNPVIYTW RSRDLRREVL
REDG4	SILLLD	STCP	VRACPVL	YKA HYFFAFATLN	SLLNPVIYTW RSRDLRREVL
	301				350
HEDG4	RPLQCWR	PGV	GVQGRRRGGT	PGHLLPLRS	SSSLERGMHM PTSPTFLEGN
HEDG4#36	RPLQCWR	PGV	GVQGRRRGGT	PGHLLPLRS	SSSLERGMHM PTSPTFLEGN
REDG4	RPLLCWR	QGK	GATG.RRG	CN PGHLLPLRS	SSSLERGLHM PTSPTFLEGN
	351				
HEDG4	TVV-				
HEDG4#36	TVV-				
REDG4	TVV-				

Figure 18A.



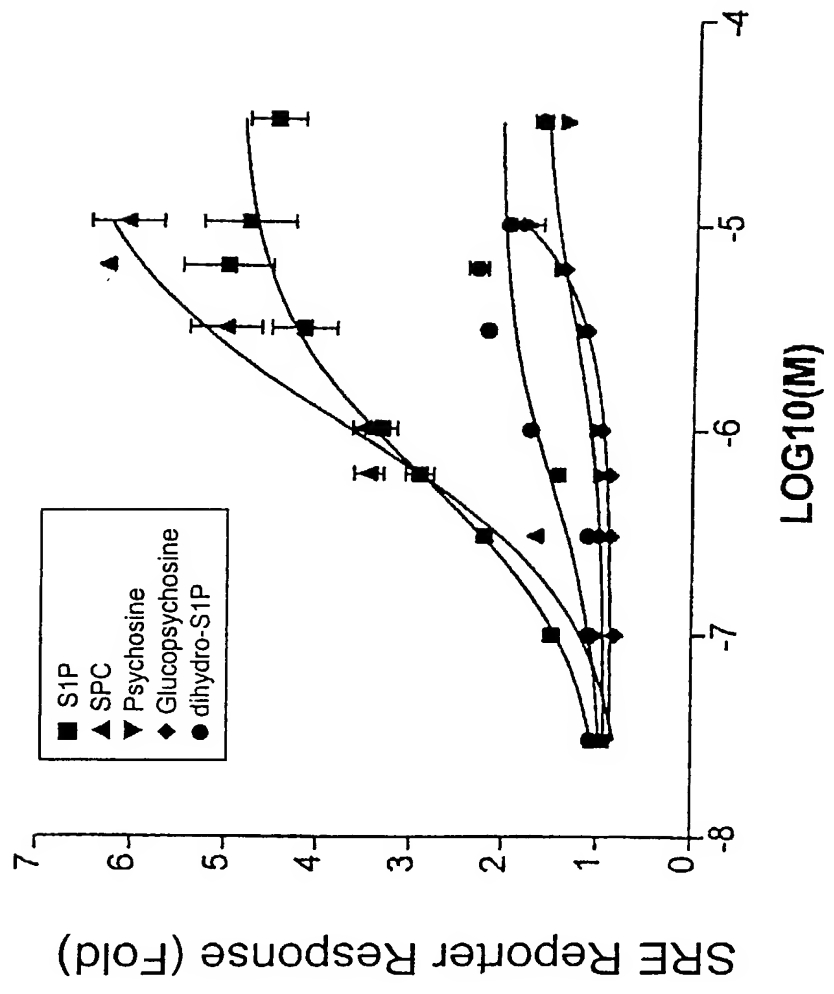
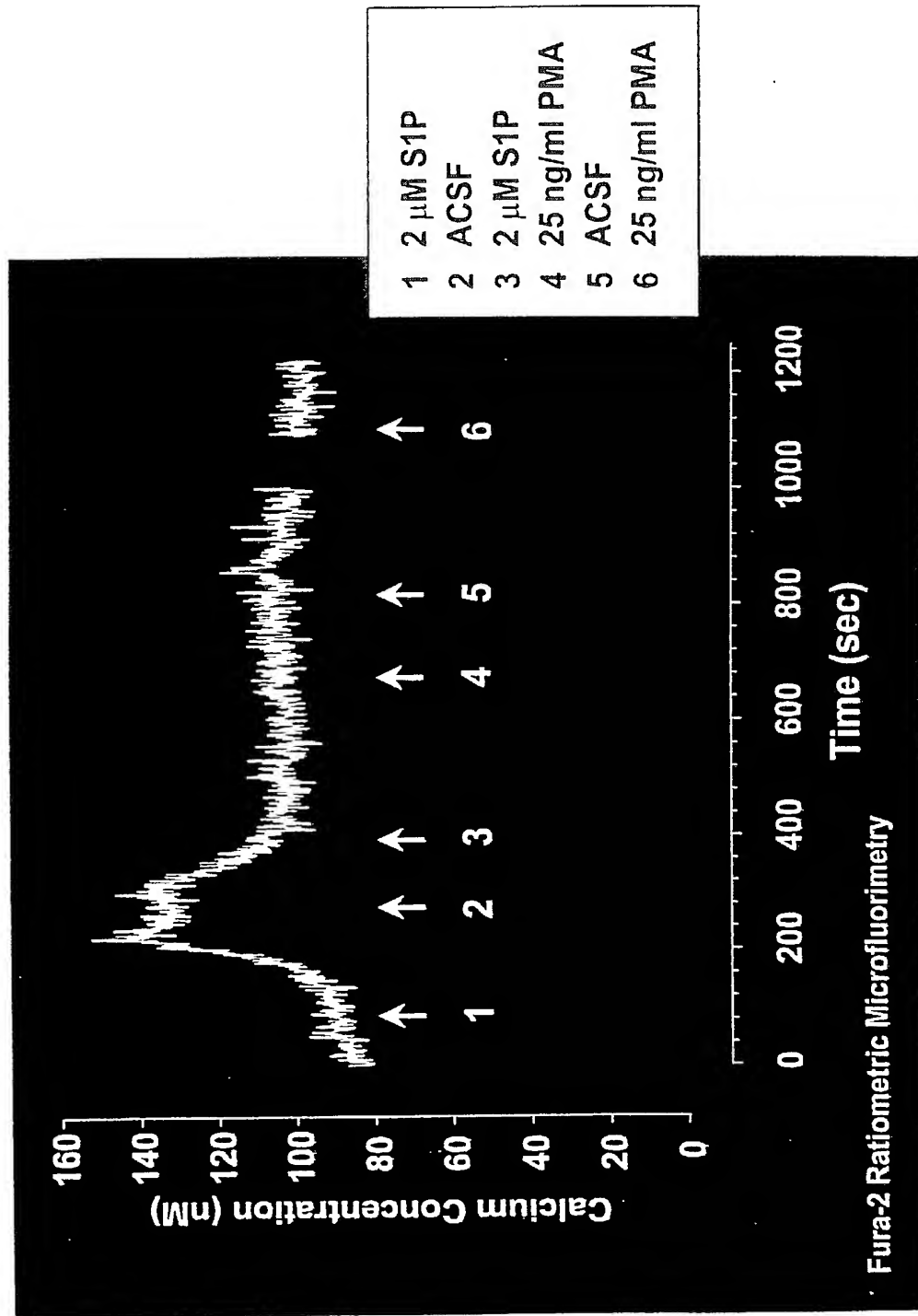


Figure 18B.

Figure 19.



10094507-051402

Figure 20.

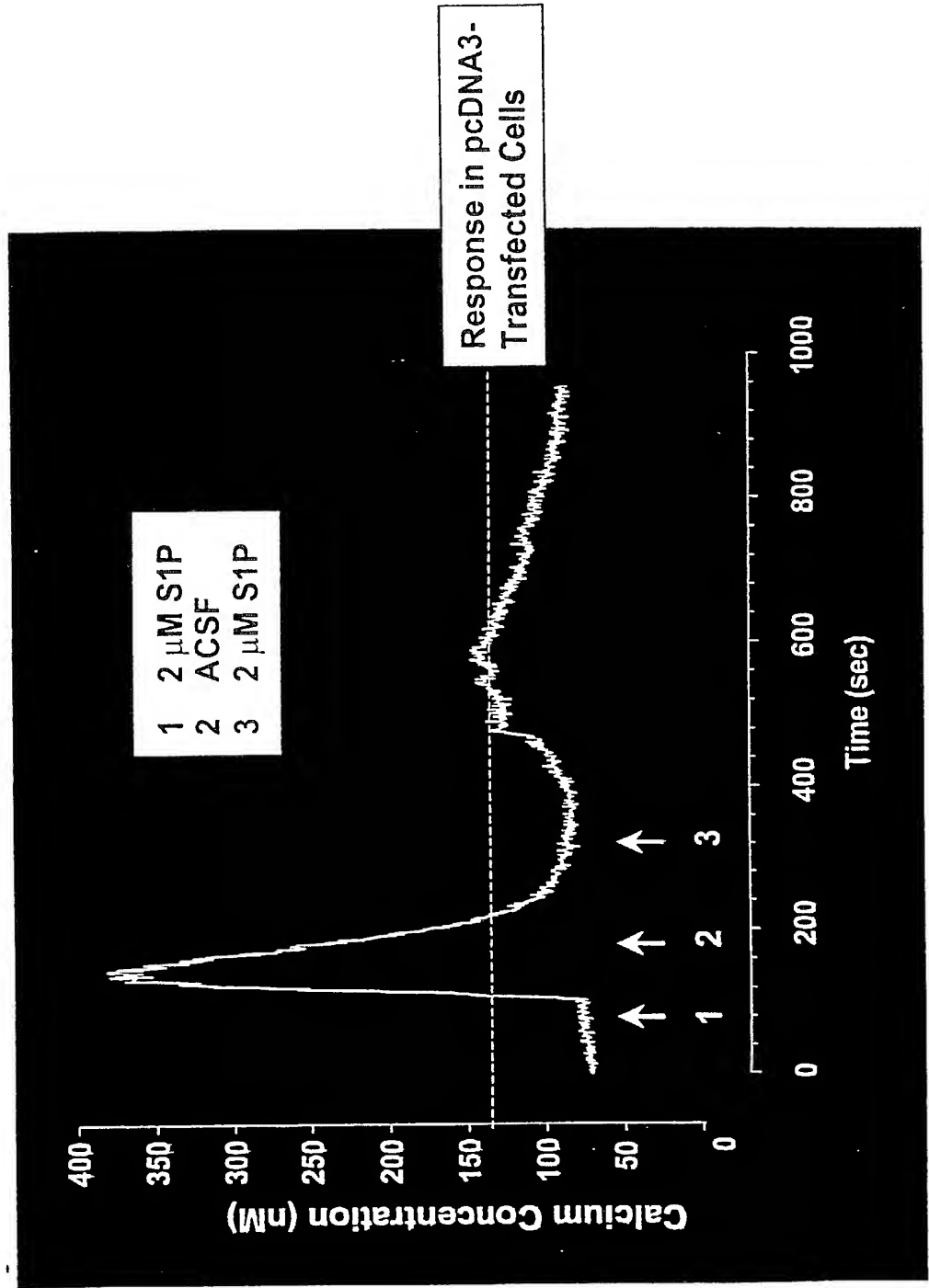


Figure 21. Human Edg-6 Amino Acid Sequence.

```

      MVIMGQCYNETIGFFYNNSGKELSSHWRPKDVVVVALGLTVSVLVLLTNLLVIAAIASN
1  -----+-----+-----+-----+-----+-----+
                                     60
      RRFHQPIYYLLGNLAAADLFAGVAYLFLMFHTGPRTARLSLEGWFLRQGLLDTSLTASVA
61 -----+-----+-----+-----+-----+-----+
                                     120
      TLLAIAVERHRSVMAVQLHSRLPRGRVVMLIVGVVVAALGLGLLPAHSWHCLCALDRCSR
121 -----+-----+-----+-----+-----+-----+
                                     180
      MAPLLSRSYLAVWALSSLLVFLLMVAVYTRIFFYVRRRVQMAEHVSCHPRYRETTLSLV
181 -----+-----+-----+-----+-----+-----+
                                     240
      KTVVIIILGAFVVCWTPGQVVLDDGLGCESC�VLAVEKYFLLAEANSLVNAAVYSCRDA
241 -----+-----+-----+-----+-----+-----+
                                     300
      EMRRTFRRLCCACLRQSTRESVHYTSSAQGGASTRIMLPENGHPLMDSTL*
301 -----+-----+-----+-----+-----+-----+
                                     352

```

Figure 22. Human Edg-6 Sequence

```

1  ATGGTCATCATGGGCCAGTGCTACTACAACGAGACCATCGGCTTCTTCTATAACAACAGT
   -----+-----+-----+-----+-----+-----+-----+
61 TACCAGTAGTACCCGGTCACGATGATGTTGCTCTGGTAGCCGAAGAAGATATTGTTGTCA
   -----+-----+-----+-----+-----+-----+-----+
   GGCAAAGAGCTCAGCTCCCACTGGCGGCCCAAGGATGTGGTCGTGGTGGCACTGGGGCTG
   -----+-----+-----+-----+-----+-----+-----+
121 CCGTTTCTCGAGTCGAGGGTGACCGCCGGGTTCTTACACCAGCACCACCGTGACCCGAC
   -----+-----+-----+-----+-----+-----+-----+
   ACCGTCAGCGTGCTGGTGCTGCTGACCAATCTGCTGGTCATAGCAGCCATCGCCTCCAAC
   -----+-----+-----+-----+-----+-----+-----+
181 TGGCAGTCGCACGACCACGACGACTGGTTAGACGACCAGTATCGTCGGTAGCGGAGGTTG
   -----+-----+-----+-----+-----+-----+-----+
   CGCCGCTTCCACCAGCCCATCTACTACCTGCTCGGCAATCTGGCCGCGGCTGACCTCTTC
   -----+-----+-----+-----+-----+-----+-----+
241 GCGGCGAAGGTGGTCGGGTAGATGATGGACGAGCCGTTAGACCGGCGCCGACTGGAGAAG
   -----+-----+-----+-----+-----+-----+-----+
   GCGGGCGTGCCCTACCTCTTCTCATGTTCCACACTGGTCCCCGCACAGCCCGACTTTCA
   -----+-----+-----+-----+-----+-----+-----+
301 CGCCCGCACCCGATGGAGAAGGAGTACAAGGTGTGACCAGGGGCGTGTGCGGCTGAAAGT
   -----+-----+-----+-----+-----+-----+-----+
   CTTGAGGGCTGGTTCTTCTGCGGCAGGGCTTGCTGGACACAAGCCTCACTGCGTCGGTGGCC
   -----+-----+-----+-----+-----+-----+-----+
361 GAACTCCCCGACCAAGGACGCCGTCCCGAACGACCTGTGTTTCGGAGTGACGCAGCCACCGG
   -----+-----+-----+-----+-----+-----+-----+
   ACACTGCTGGCCATCGCCGTGGAGCGGCACCGCAGTGTGATGGCCGTGCAGCTGCACAGC
   -----+-----+-----+-----+-----+-----+-----+
421 TGTGACGACCCGTAGCGGCACCTCGCCGTGGCGTCACACTACCGGCACGTGACGTGTGCG
   -----+-----+-----+-----+-----+-----+-----+
   CGCCTGCCCCGTGGCCGCGTGGTCATGCTCATTGTGGGCGTGTGGGTGGCTGCCCTGGGC
   -----+-----+-----+-----+-----+-----+-----+
481 GCGGACGGGGCACCGGCGCACCAGTACGAGTAACACCCGCACACCCACCGACGGGACCCG
   -----+-----+-----+-----+-----+-----+-----+
   CTGGGGCTGCTGCCTGCCCCTCTGGCACTGCCTCTGTGCCCTGGACCGCTGCTCACGC
   -----+-----+-----+-----+-----+-----+-----+
541 GACCCCGACGACGGACGGGTGAGGACCGTGACGGAGACACGGGACCTGGCGACGAGTGCG
   -----+-----+-----+-----+-----+-----+-----+
   ATGGCACCCCTGCTCAGCCGCTCCTATTTGGCCGTCTGGGCTCTGTGAGCCTGCTTGTC
   -----+-----+-----+-----+-----+-----+-----+
601 TACCGTGGGGACGAGTCGGCGAGGATAAACCGGCAGACCCGAGACAGCTCGGACGAACAG
   -----+-----+-----+-----+-----+-----+-----+
   TTCCTGCTCATGGTGGCTGTGTACACCCGATTTTCTTCTACGTGCGGCGGCGAGTGCAG
   -----+-----+-----+-----+-----+-----+-----+
661 AAGGACGAGTACCACCGACACATGTGGGCGTAAAAGAAGATGCACGCCGCCGCTCACGTC
   -----+-----+-----+-----+-----+-----+-----+
   CGCATGGCAGAGCATGTCAGCTGCCACCCCGCTACCGAGAGACCACGCTCAGCCTGGTC
   -----+-----+-----+-----+-----+-----+-----+
721 GCGTACCGTCTCGTACAGTCGACGGTGGGGCGATGGCTCTCTGGTGCGAGTCGGACCAG
   -----+-----+-----+-----+-----+-----+-----+
   AAGACTGTTGTTCATCATCCTGGGGGCGTTCGTGGTCTGCTGGACACCAGGCCAGGTGGTA
   -----+-----+-----+-----+-----+-----+-----+
781 TTCTGACAACAGTAGTAGGACCCCCGCAAGCACCAGACGACCTGTGGTCCGGTCCACCAT
   -----+-----+-----+-----+-----+-----+-----+
   CTGCTCCTGGATGGTTTAGGCTGTGAGTCCTGCAATGTCTGGCTGTAGAAAAGTACTTC
   -----+-----+-----+-----+-----+-----+-----+
840 GACGAGGACCTACCAAATCCGACACTCAGGACGTTACAGGACCGACATCTTTTCATGAAG

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      CTACTGcTGGCCGAGGCCAACTCACTGGTCAATGCTGCTGTGTACTCTTGCCGAGATGCT
841  -----+-----+-----+-----+-----+-----+
      GATGACgACCGGCTCCGGTTGAGTGACCAGTTACGACGACACATGAGAACGGCTCTACGA
                                     900

      GAGATGCGCCGCACCTTCCGCCGCCTTCTCTGCTGCGCGTGCC'TCCGCCAGTCCACCCGC
901  -----+-----+-----+-----+-----+-----+
      CTCTACGCGGCGTGGAAGGCGGCGGAAGAGACGACGCGCACGGAGGCGGTCAGGTGGGCG
                                     960

      GAGTCTGTCCACTATACATCCTCTGCCCAGGGAGGTGCCAGCACTCGCATCATGCTTCCC
961  -----+-----+-----+-----+-----+-----+
      CTCAGACAGGTGATATGTAGGAGACGGGTCCCTCCACGGTCGTGAGCGTAGTACGAAGGG
                                     1020

      GAGAACGGCCACCCACTGATGGACTCCACCCTTTAG
1021 -----+-----+-----+-----+-----+
      CTCTTGCCGGTGGGTGACTACCTGAGGTGGGAAATC
                                     1056

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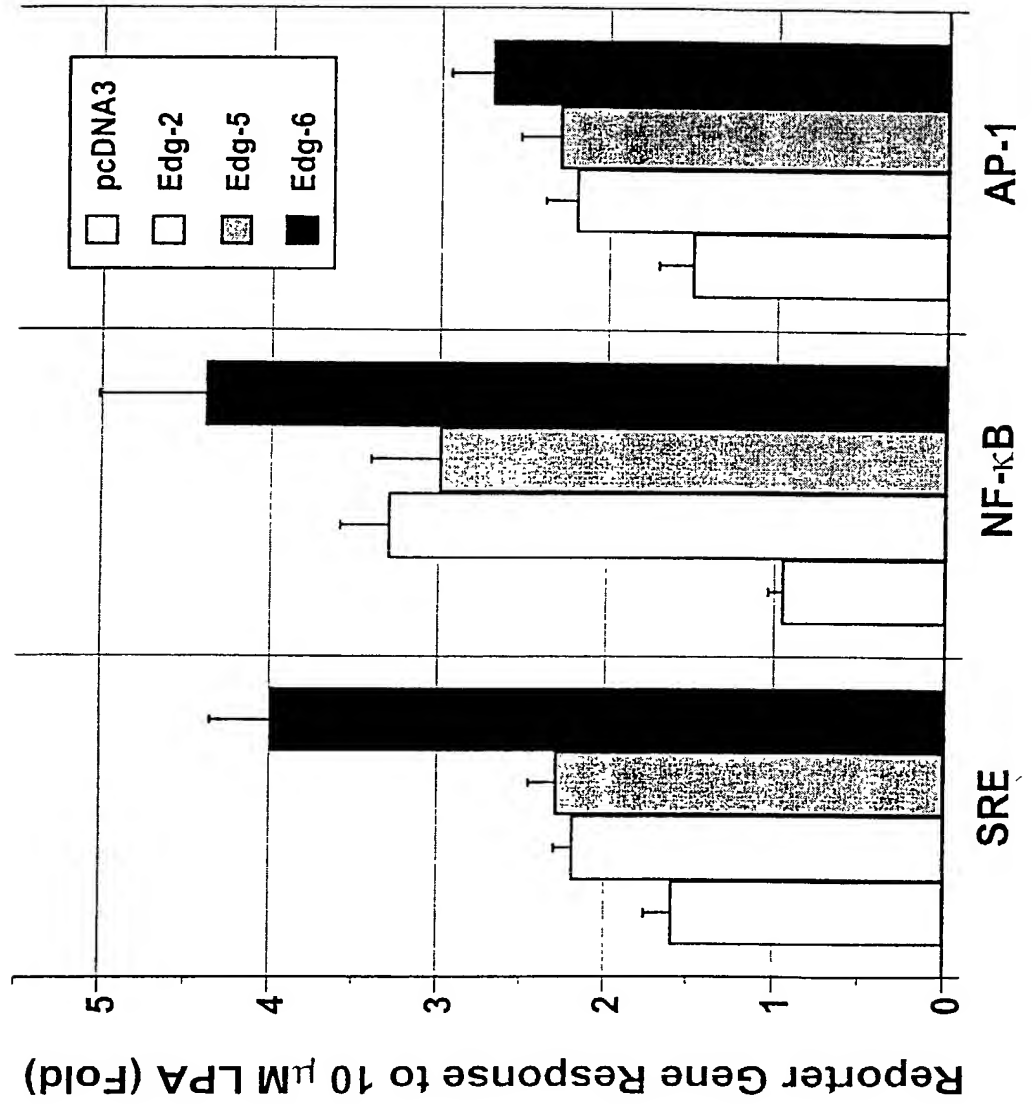


Figure 23.

Figure 24.

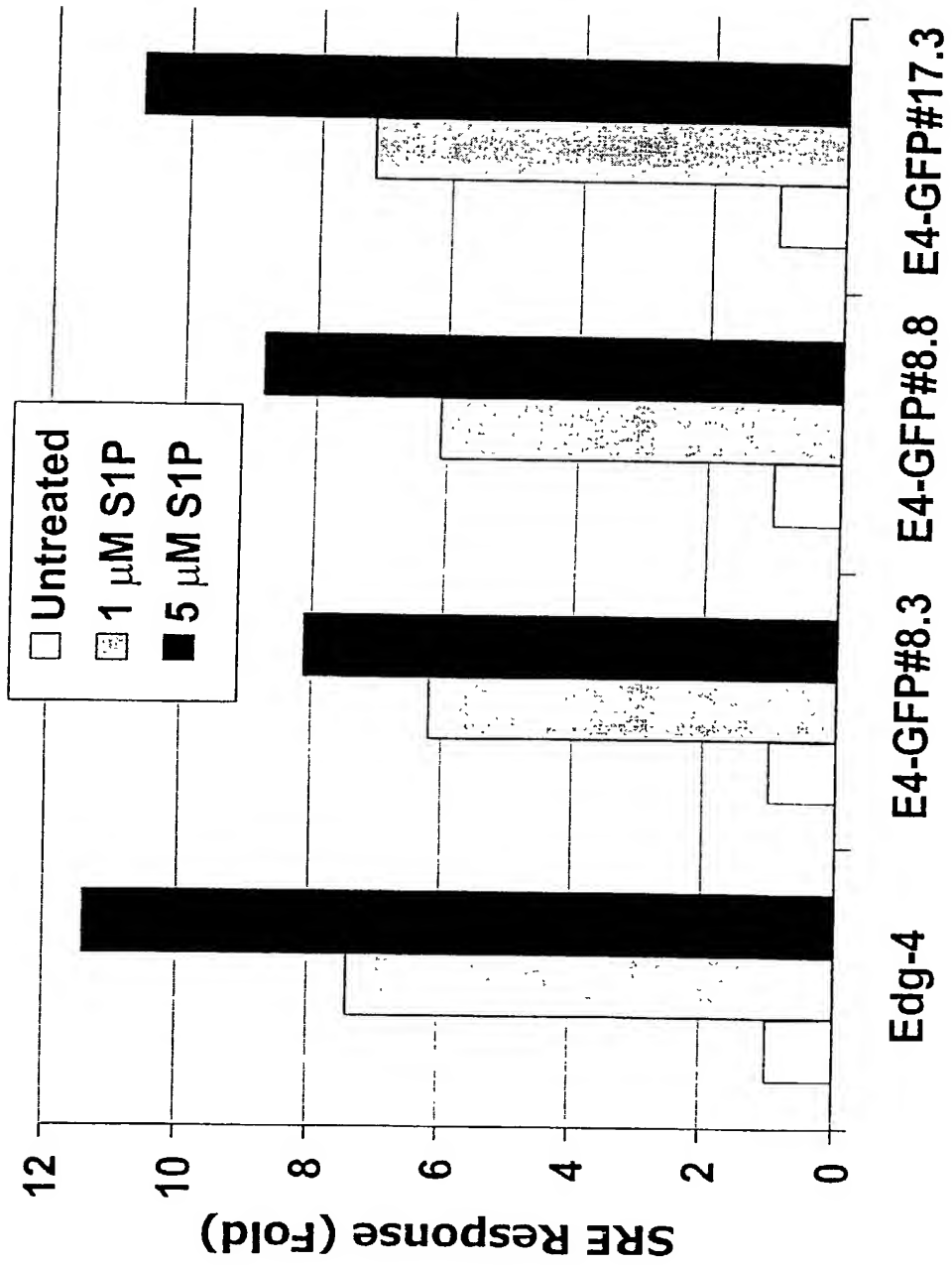


Figure 25.

